04CO

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RAW SEQUENCE LISTING   DATE: 03/01/2001
PATENT APPLICATION: US/09/775,009   TIME: 09:37:54

Input Set : A:\Seqlist.txt
Output Set: N:\CRF3\02282001\I775009.raw

ENTERED

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 3 <110> APPLICANT: Chiang, Lillian Wei-Ming
 5 <120> TITLE OF INVENTION: NARC8 Programmed Cell Death-Associated
 6         Molecule and Uses Thereof
10 <130> FILE REFERENCE: 35800/207197
C--> 12 <140> CURRENT APPLICATION NUMBER: US/09/775,009
C--> 12 <141> CURRENT FILING DATE: 2001-02-01
12 <150> PRIOR APPLICATION NUMBER: 09/692,785
13 <151> PRIOR FILING DATE: 2000-10-20
15 <150> PRIOR APPLICATION NUMBER: 60/161,188
16 <151> PRIOR FILING DATE: 1999-10-22
18 <160> NUMBER OF SEQ ID NOS: 7
20 <170> SOFTWARE: FastSEQ for Windows Version 4.0
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23 <211> LENGTH: 1507
24 <212> TYPE: DNA
25 <213> ORGANISM: Homo sapiens
27 <220> FEATURE:
28 <221> NAME/KEY: CDS
29 <222> LOCATION: (368)...(1261)
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33 tggcgggggc tgctcccagc ttctggctgt cacggacctg ccgcctcctc ctactccgca     120
34 tccgccgagc ctgcccgggt ccgggcgctt gtctatgggc accacgggga tccagccaag     180
35 gtcgtcgaaa ccgtaattcc tgggcacaca tggcagctca gaaatgttgc ctgacctact     240
36 ttgaggagat gatttgagcg aaacacccat tctagcctgg atgacatgaa catctccgtt     300
37 tggctttgtg cttagactca agaacctgga gctagctgct gtgagaggat cagatgtccg     360
38 tgtgaag atg ctg gcg gcc cct atc aat cca tct gac ata aat atg atc      409
39          Met Leu Ala Ala Pro Ile Asn Pro Ser Asp Ile Asn Met Ile
40            1          5              10
42 caa gga aac tac gga ctc ctt cct gaa ctg cct gct gtt gga ggg aac      457
43 Gln Gly Asn Tyr Gly Leu Leu Pro Glu Leu Pro Ala Val Gly Gly Asn
44  15              20              25              30
46 gaa ggt gtt gca cag gtg gta gcg gtg ggc agc aat gtg acc ggg ctg      505
47 Glu Gly Val Ala Gln Val Val Ala Val Gly Ser Asn Val Thr Gly Leu
48              35              40              45
50 aag cca gga gac tgg gtg att cca gca aat gct ggt tta gga acc tgg      553
51 Lys Pro Gly Asp Trp Val Ile Pro Ala Asn Ala Gly Leu Gly Thr Trp
52              50              55              60
54 cgg acc gag gct gtg ttc agc gag gaa gca ctg atc caa gtt ccg agt      601
55 Arg Thr Glu Ala Val Phe Ser Glu Glu Ala Leu Ile Gln Val Pro Ser
56              65              70              75
58 gac atc cct ctt cag agc gct gcc acc ctg ggt gtc aat ccc tgc aca      649
59 Asp Ile Pro Leu Gln Ser Ala Ala Thr Leu Gly Val Asn Pro Cys Thr
60       80              85              90
62 gcc tac agg atg ttg atg gat ttc gag caa ctg cag cca ggg gat tct      697
63 Ala Tyr Arg Met Leu Met Asp Phe Glu Gln Leu Gln Pro Gly Asp Ser
64  95              100             105             110
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66  gtc atc cag aat gca tcc aac agc gga gtg ggg caa gcg gtc atc cag       745
67  Val Ile Gln Asn Ala Ser Asn Ser Gly Val Gly Gln Ala Val Ile Gln
68              115                 120                 125
70  atc gcc gca gcc ctg ggc cta aga acc atc aat gtg gtc cga gac aga       793
71  Ile Ala Ala Ala Leu Gly Leu Arg Thr Ile Asn Val Val Arg Asp Arg
72              130                 135                 140
74  cct gat atc cag aag ctg agt gac aga ctg aag agt ctg ggg gct gag       841
75  Pro Asp Ile Gln Lys Leu Ser Asp Arg Leu Lys Ser Leu Gly Ala Glu
76          145                 150                 155
78  cat gtc atc aca gaa gag gag cta aga agg ccc gaa atg aaa aac ttc       889
79  His Val Ile Thr Glu Glu Glu Leu Arg Arg Pro Glu Met Lys Asn Phe
80          160                 165                 170
82  ttt aag gac atg ccc cag cca cgg ctt gct ctc aac tgt gtt ggt ggg       937
83  Phe Lys Asp Met Pro Gln Pro Arg Leu Ala Leu Asn Cys Val Gly Gly
84  175                 180                 185                 190
86  aaa agc tcc aca gag ctg ctg cgg cag tta gcg cgt gga gga acc atg       985
87  Lys Ser Ser Thr Glu Leu Leu Arg Gln Leu Ala Arg Gly Gly Thr Met
88              195                 200                 205
90  gta acc tat ggg ggg atg gcc aag cag ccc gtc gta gcc tct gtg agc      1033
91  Val Thr Tyr Gly Gly Met Ala Lys Gln Pro Val Val Ala Ser Val Ser
92              210                 215                 220
94  ctg ctc att ttt aag gat ctc aaa ctt cga ggc ttt tgg ttg tcc cag      1081
95  Leu Leu Ile Phe Lys Asp Leu Lys Leu Arg Gly Phe Trp Leu Ser Gln
96              225                 230                 235
98  tgg aag aag gat cac agt cca gac cag ttc aag gag ctg atc ctc aca      1129
99  Trp Lys Lys Asp His Ser Pro Asp Gln Phe Lys Glu Leu Ile Leu Thr
100         240                 245                 250
102 ctg tgc gat ctc atc cgc cga ggc cag ctc aca gcc cct gcc tgc tcc      1177
103 Leu Cys Asp Leu Ile Arg Arg Gly Gln Leu Thr Ala Pro Ala Cys Ser
104 255                 260                 265                 270
106 cag gtc ccg ctg cag gac tac cag tct gcc ttg gaa gcc tcc atg aag      1225
107 Gln Val Pro Leu Gln Asp Tyr Gln Ser Ala Leu Glu Ala Ser Met Lys
108             275                 280                 285
110 ccc ttc ata tct tca aag cag att ctc acc atg tga tcatcccaaa           1271
111 Pro Phe Ile Ser Ser Lys Gln Ile Leu Thr Met  *
112             290                 295
114 agagctggag tgacatggga ggggaggcgg atctgagggg ctgggtgcag gcccctcagt    1331
115 tggggctccc accttcccca gactactgtt ctcctcactg cctcttccta ttaggaggat    1391
116 ggtgaagcca gccacggttt tccccagggc cagccttaag gtatctaata aagtctgaac    1451
117 tctcccttcc aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa         1507
119 <210> SEQ ID NO: 2
120 <211> LENGTH: 297
121 <212> TYPE: PRT
122 <213> ORGANISM: Homo sapiens
124 <400> SEQUENCE: 2
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126 1               5                   10                  15
127 Asn Tyr Gly Leu Leu Pro Glu Leu Pro Ala Val Gly Gly Asn Glu Gly
128             20                  25                  30
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129 Val Ala Gln Val Val Ala Val Gly Ser Asn Val Thr Gly Leu Lys Pro
130         35              40              45
131 Gly Asp Trp Val Ile Pro Ala Asn Ala Gly Leu Gly Thr Trp Arg Thr
132     50              55              60
133 Glu Ala Val Phe Ser Glu Glu Ala Leu Ile Gln Val Pro Ser Asp Ile
134 65              70              75              80
135 Pro Leu Gln Ser Ala Ala Thr Leu Gly Val Asn Pro Cys Thr Ala Tyr
136         85              90              95
137 Arg Met Leu Met Asp Phe Glu Gln Leu Gln Pro Gly Asp Ser Val Ile
138         100             105             110
139 Gln Asn Ala Ser Asn Ser Gly Val Gly Gln Ala Val Ile Gln Ile Ala
140     115             120             125
141 Ala Ala Leu Gly Leu Arg Thr Ile Asn Val Val Arg Asp Arg Pro Asp
142     130             135             140
143 Ile Gln Lys Leu Ser Asp Arg Leu Lys Ser Leu Gly Ala Glu His Val
144 145             150             155             160
145 Ile Thr Glu Glu Glu Leu Arg Arg Pro Glu Met Lys Asn Phe Phe Lys
146         165             170             175
147 Asp Met Pro Gln Pro Arg Leu Ala Leu Asn Cys Val Gly Gly Lys Ser
148         180             185             190
149 Ser Thr Glu Leu Leu Arg Gln Leu Ala Arg Gly Gly Thr Met Val Thr
150     195             200             205
151 Tyr Gly Gly Met Ala Lys Gln Pro Val Val Ala Ser Val Ser Leu Leu
152     210             215             220
153 Ile Phe Lys Asp Leu Lys Leu Arg Gly Phe Trp Leu Ser Gln Trp Lys
154 225             230             235             240
155 Lys Asp His Ser Pro Asp Gln Phe Lys Glu Leu Ile Leu Thr Leu Cys
156         245             250             255
157 Asp Leu Ile Arg Arg Gly Gln Leu Thr Ala Pro Ala Cys Ser Gln Val
158         260             265             270
159 Pro Leu Gln Asp Tyr Gln Ser Ala Leu Glu Ala Ser Met Lys Pro Phe
160     275             280             285
161 Ile Ser Ser Lys Gln Ile Leu Thr Met
162     290             295
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165 <211> LENGTH: 894
166 <212> TYPE: DNA
167 <213> ORGANISM: Homo sapiens
169 <400> SEQUENCE: 3
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171 cttcctgaac tgcctgctgt tggagggaac gaaggtgttg cacaggtggt agcggtgggc     120
172 agcaatgtga ccgggctgaa gccaggagac tgggtgattc cagcaaatgc tggtttagga     180
173 acctggcgga ccgaggctgt gttcagcgag gaagcactga tccaagttcc gagtgacatc     240
174 cctcttcaga gcgctgccac cctgggtgtc aatccctgca cagcctacag gatgttgatg     300
175 gatttcgagc aactgcagcc aggggattct gtcatccaga atgcatccaa cagcggagtg     360
176 gggcaagcgg tcatccagat cgccgcagcc ctgggcctaa gaaccatcaa tgtggtccga     420
177 gacagacctg atatccagaa gctgagtgac agactgaaga gtctgggggc tgagcatgtc     480
178 atcacagaag aggagctaag aaggcccgaa atgaaaaact tctttaagga catgccccag     540
179 ccacggcttg ctctcaactg tgttggtggg aaaagctcca cagagctgct gcggcagtta     600
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          Input Set : A:\Seqlist.txt
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180 gcgcgtggag gaaccatggt aacctatggg gggatggcca agcagcccgt cgtagcctct       660
181 gtgagcctgc tcatttttaa ggatctcaaa cttcgaggct tttggttgtc ccagtggaag       720
182 aaggatcaca gtccagacca gttcaaggag ctgatcctca cactgtgcga tctcatccgc       780
183 cgaggccagc tcacagcccc tgcctgctcc caggtcccgc tgcaggacta ccagtctgcc       840
184 ttggaagcct ccatgaagcc cttcatatct tcaaagcaga ttctcaccat gtga             894
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187 <211> LENGTH: 1380
188 <212> TYPE: DNA
189 <213> ORGANISM: Homo sapiens
191 <220> FEATURE:
192 <221> NAME/KEY: CDS
193 <222> LOCATION: (13)...(1134)
195 <400> SEQUENCE: 4
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197                Met Trp Val Cys Ser Thr Leu Trp Arg Val Arg Thr Pro
198                 1               5                  10
200 gcc cgg cag tgg cgg ggg ctg ctc cca gct tct ggc tgt cac gga cct          99
201 Ala Arg Gln Trp Arg Gly Leu Leu Pro Ala Ser Gly Cys His Gly Pro
202    15               20              25
204 gcc gcc tcc tcc tac tcc gca tcc gcc gag cct gcc cgg gtc cgg gcg         147
205 Ala Ala Ser Ser Tyr Ser Ala Ser Ala Glu Pro Ala Arg Val Arg Ala
206  30               35              40                  45
208 ctt gtc tat ggg cac cac ggg gat cca gcc aag gtc gtc gaa ctc aag         195
209 Leu Val Tyr Gly His His Gly Asp Pro Ala Lys Val Val Glu Leu Lys
210                  50              55                  60
212 aac ctg gag cta gct gct gtg aga gga tca gat gtc cgt gtg aag atg         243
213 Asn Leu Glu Leu Ala Ala Val Arg Gly Ser Asp Val Arg Val Lys Met
214                  65              70                  75
216 ctg gcg gcc cct atc aat cca tct gac ata aat atg atc caa gga aac         291
217 Leu Ala Ala Pro Ile Asn Pro Ser Asp Ile Asn Met Ile Gln Gly Asn
218             80              85              90
220 tac gga ctc ctt cct gaa ctg cct gct gtt gga ggg aac gaa ggt gtt         339
221 Tyr Gly Leu Leu Pro Glu Leu Pro Ala Val Gly Gly Asn Glu Gly Val
222     95              100             105
224 gca cag gtg gta gcg gtg ggc agc aat gtg acc ggg ctg aag cca gga         387
225 Ala Gln Val Val Ala Val Gly Ser Asn Val Thr Gly Leu Lys Pro Gly
226 110             115             120                 125
228 gac tgg gtg att cca gca aat gct ggt tta gga acc tgg cgg acc gag         435
229 Asp Trp Val Ile Pro Ala Asn Ala Gly Leu Gly Thr Trp Arg Thr Glu
230             130             135             140
232 gct gtg ttc agc gag gaa gca ctg atc caa gtt ccg agt gac atc cct         483
233 Ala Val Phe Ser Glu Glu Ala Leu Ile Gln Val Pro Ser Asp Ile Pro
234          145             150             155
236 ctt cag agc gct gcc acc ctg ggt gtc aat ccc tgc aca gcc tac agg         531
237 Leu Gln Ser Ala Ala Thr Leu Gly Val Asn Pro Cys Thr Ala Tyr Arg
238          160             165             170
240 atg ttg atg gat ttc gag caa ctg cag cca ggg gat tct gtc atc cag         579
241 Met Leu Met Asp Phe Glu Gln Leu Gln Pro Gly Asp Ser Val Ile Gln
242     175             180             185
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244 aat gca tcc aac agc gga gtg ggg caa gcg gtc atc cag atc gcc gca     627
245 Asn Ala Ser Asn Ser Gly Val Gly Gln Ala Val Ile Gln Ile Ala Ala
246 190             195             200             205
248 gcc ctg ggc cta aga acc atc aat gtg gtc cga gac aga cct gat atc     675
249 Ala Leu Gly Leu Arg Thr Ile Asn Val Val Arg Asp Arg Pro Asp Ile
250             210             215             220
252 cag aag ctg agt gac aga ctg aag agt ctg ggg gct gag cat gtc atc     723
253 Gln Lys Leu Ser Asp Arg Leu Lys Ser Leu Gly Ala Glu His Val Ile
254             225             230             235
256 aca gaa gag gag cta aga agg ccc gaa atg aaa aac ttc ttt aag gac     771
257 Thr Glu Glu Glu Leu Arg Arg Pro Glu Met Lys Asn Phe Phe Lys Asp
258         240             245             250
260 atg ccc cag cca cgg ctt gct ctc aac tgt gtt ggt ggg aaa agc tcc     819
261 Met Pro Gln Pro Arg Leu Ala Leu Asn Cys Val Gly Gly Lys Ser Ser
262     255             260             265
264 aca gag ctg ctg cgg cag tta gcg cgt gga gga acc atg gta acc tat     867
265 Thr Glu Leu Leu Arg Gln Leu Ala Arg Gly Gly Thr Met Val Thr Tyr
266 270             275             280             285
268 ggg ggg atg gcc aag cag ccc gtc gta gcc tct gtg agc ctg ctc att     915
269 Gly Gly Met Ala Lys Gln Pro Val Val Ala Ser Val Ser Leu Leu Ile
270             290             295             300
272 ttt aag gat ctc aaa ctt cga ggc ttt tgg ttg tcc cag tgg aag aag     963
273 Phe Lys Asp Leu Lys Leu Arg Gly Phe Trp Leu Ser Gln Trp Lys Lys
274             305             310             315
276 gat cac agt cca gac cag ttc aag gag ctg atc ctc aca ctg tgc gat     1011
277 Asp His Ser Pro Asp Gln Phe Lys Glu Leu Ile Leu Thr Leu Cys Asp
278             320             325             330
280 ctc atc cgc cga ggc cag ctc aca gcc cct gcc tgc tcc cag gtc ccg     1059
281 Leu Ile Arg Arg Gly Gln Leu Thr Ala Pro Ala Cys Ser Gln Val Pro
282     335             340             345
284 ctg cag gac tac cag tct gcc ttg gaa gcc tcc atg aag ccc ttc ata     1107
285 Leu Gln Asp Tyr Gln Ser Ala Leu Glu Ala Ser Met Lys Pro Phe Ile
286 350             355             360             365
288 tct tca aag cag att ctc acc atg tga tcatcccaaa agagctggag     1154
289 Ser Ser Lys Gln Ile Leu Thr Met  *
290             370
292 tgacatggga ggggaggcgg atctgagggg ctgggtgcag gcccctcagt tggggctccc     1214
293 accttcccca gactactgtt ctcctcactg cctcttccta ttaggaggat ggtgaagcca     1274
294 gccacggttt tccccagggc cagccttaag gtatctaata aagtctgaac tctcccttcc     1334
295 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa     1380
297 <210> SEQ ID NO: 5
298 <211> LENGTH: 373
299 <212> TYPE: PRT
300 <213> ORGANISM: Homo sapiens
302 <400> SEQUENCE: 5
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304  1             5             10             15
305 Trp Arg Gly Leu Leu Pro Ala Ser Gly Cys His Gly Pro Ala Ala Ser
306             20             25             30
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L:12 M:270 C: Current Application Number differs, Replaced Current Application No
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date

NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 C.F.R. 1.821 - 1.825 for the following reason(s):

☐ 1. This application clearly fails to comply with the requirements of 37 C.F.R. 1.821-1.825. Applicant's attention is directed to these regulations, published at 1114 OG 29, May 15, 1990 and at 55 FR 18230, May 1, 1990.

☐ 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 C.F.R. 1.821(c).

☒ 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 C.F.R. 1.821(e).

☐ 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked-up "Raw Sequence Listing."

☐ 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A Substitute computer readable form must be submitted as required by 37 C.F.R. 1.825(d).

☐ 6. The paper copy of the "Sequence Listing" is not the same as the computer readable form of the "Sequence Listing" as required by 37 C.F.R. 1.821(e).

☐ 7. Other: _____

Applicant Must Provide:

☒ An initial or substitute computer readable form (CRF) copy of the "Sequence Listing".

☐ An initial or substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification.

☒ A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 C.F.R. 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d).

For questions regarding compliance to these requirements, please contact:

For Rules Interpretation, call (703) 308-4216
For CRF Submission Help, call (703) 308-4212
For PatentIn software help, call (703) 308-6856

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